



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102806

TO: Minh-Tam Davis
Location: CM1/8A01&8E12
Art Unit: 1642

Sept 6, 2003

Case Serial Number: 09/700700

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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STIC-Biotech/Ch mLib

102806

From: Chan, Christina
Sent: Saturday, August 30, 2003 9:39 AM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/700700

Please ~~rush~~: Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Davis, Minh-Tam
Sent: Friday, August 29, 2003 10:49 AM
T : Chan, Christina
Subject: Rush search request for 09/700700

1) Please search SEQ ID NO:335 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL_ID=09439313>

is a continuation in part of 09352616 <snquery.pl?APPL_ID=09352616>

Which is a continuation in part of 09288946 <snquery.pl?APPL_ID=09288946>

Which is a continuation in part of 09232149 <snquery.pl?APPL_ID=09232149>

Which is a continuation in part of 09159812 <snquery.pl?APPL_ID=09159812>

Which is a continuation in part of 09115453 <snquery.pl?APPL_ID=09115453>

Which is a continuation in part of 09030607 <snquery.pl?APPL_ID=09030607>

Which is a continuation in part of 09020956 <snquery.pl?APPL_ID=09020956>

Which is a continuation in part of 08904804 <snquery.pl?APPL_ID=08904804>

Which is a continuation in part of 08806099 <snquery.pl?APPL_ID=08806099>

? leave # 335
to 7/14/98 file date
Same as # 115
Leave both file 2/25/98
part of # 335
do not leave any
part of # 335

1) Please search SEQ ID NO:1 of the instant application against the sequences of 20030022275 (or US 6617129) and 60/051080

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

11
STN = 09/105,470

Point of Contact
P. Sheppard
telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 9/6/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 439313-335Xlist.res made by spaula on Wed 3 Sep 103 16:22:11-PDT.

Query sequence being compared:	US-09-439-313-335 (1-2984)
Number of sequences searched:	2159
Number of scores above cutoff:	2159

Results of the initial comparison of US-09-439-313-335 (1-2984) with:

```
File : 6261562.seq
File : 6262245.seq
File : 6395278.seq
File : 6465611.seq
File : 6613872.seq
File : US08806039.seq
File : US08904804.seq
File : US09115453.seq
File : US09288946.seq
```

[illegible]

PARAMETERS

	Unary	K-tuple
Similarity matrix	1	4
Mismatch penalty	1.00	30
Gap penalty	0.33	Window size
Gap size penalty	0	500
Cutoff score	0	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
---------	------	--------	--------------------

Times:	CPU	Total Elapsed
--------	-----	---------------

Number of residues: 1042365

```
Number of sequences searched: 2159
Number of scores above cutoff: 2159
```

Number of scores above cutoff: 2159

The scores below are sorted by initial score. Significance is calculated based on initial score.

3 100% identical sequences to the query sequence were found:

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Frame
1. US-03-352-616A-3	Sequence 335, Application	2984	2984	2584	26.07 0
2. US-03-232-149A-3	Sequence 335, Application	2984	2984	2584	26.07 0
3. US-03-288-946-3	Sequence 335, Application	2984	2984	2584	26.07 0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Frame
The list of other best scores is:					

***** 2 standard deviations above mean *****

[illegible]

```

*** 1 standard deviation above mean ***
sequence 110, application 270

```

13.	US-09-033-607-20	Sequence 207	Application	332	253	318	1.84	0
14.	US-09-2352-616A-2	Sequence 207	Application	332	253	318	1.84	0
15.	US-09-2352-149A-2	Sequence 207	Application	332	253	318	1.84	0
16.	US-09-1159-812-20	Sequence 207	Application	332	253	318	1.84	0
17.	US-09-1159-453-20	Sequence 207	Application	332	253	318	1.84	0
18.	US-09-3582-964-20	Sequence 207	Application	332	253	318	1.84	0
19.	US-09-352-616A-2	Sequence 295	Application	305	215	303	1.50	0
20.	US-09-2332-149A-2	Sequence 295	Application	305	215	303	1.50	0
21.	US-09-159-812-23	Sequence 295	Application	305	215	303	1.50	0
22.	US-09-288-946-29	Sequence 295	Application	305	215	303	1.50	0
*** 0 standard deviation from mean ***								
23.	US-09-030-607-21	Sequence 216	Application	260	156	232	0.98	0
24.	US-09-352-616A-2	Sequence 216	Application	260	156	232	0.98	0
25.	US-09-2332-149A-2	Sequence 216	Application	260	156	232	0.98	0
26.	US-09-159-812-21	Sequence 216	Application	260	156	232	0.98	0
27.	US-09-1159-453-21	Sequence 216	Application	260	156	232	0.98	0
28.	US-09-1159-812-21	Sequence 216	Application	260	156	232	0.98	0
29.	US-09-288-946-21	Sequence 216	Application	260	156	232	0.98	0
30.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
31.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
32.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
33.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
34.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
35.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
36.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
37.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
38.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
39.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
40.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
41.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
42.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
43.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
44.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
45.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
46.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
47.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
48.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
49.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
50.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
51.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
52.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
53.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
54.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
55.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
56.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
57.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
58.	US-09-030-607-53	Sequence 53	Application	484	108	215	0.55	0
59.	US-							

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****      0 standard deviation from mean      ****

```

23	US-09-033-607-21	Sequence 216	260	156	232	0.98
24	US-09-352-618A-2	Sequence 216	260	156	232	0.98
25	US-09-232-149A-2	Sequence 216	260	156	232	0.98
26	US-09-159-811-21	Sequence 216	260	156	232	0.98
27	US-09-115-453-21	Sequence 216	260	156	232	0.98
28	US-09-288-944-21	Sequence 216	260	156	232	0.98
29	US-09-020-907-53	Sequence 53, Application	484	108	215	0.55
30	US-09-030-607-53	Sequence 53, Application	484	108	215	0.55
31	US-09-030-607-53	Sequence 53, Application	484	108	215	0.55

1. US-09-439-313-335 (1-2984)
US-09-352-616A-3 Sequence 335, Application US/09352616A
Sequence 335, Application US/09352616A

near
inland out
along river bank
Carroll's boat at

[illegible][illegible]

SEQ ID NO 335

LENGTH: 2984

TYPE: DNA

ORGANISM: *Homo sapien*

Initial Score	=	2984	Optimized Score	=	2984	Significance	=	26.07
Residue Identity	=	100%	Matches	=	2984	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			

X 10 20 30 40 50 60 70
ATCCTCTCTTCCCACTTCTCTTCCAGAAAGCAGCTTGGGGCTTATCTGTGTGACTGTAAACAATTCA
ATCCTCTCTTCCCACTTCTCTTCCAGAAAGCAGCTTGGGGCTTATCTGTGTGACTGTAAACAATTCA
X 10 20 30 40 50 60 70
GGGCGCTTCCAAAGGCTTCTCCAAACCCCTTAAAGACCGCGAGAAAGCTCCCGAGCTCTTCTCCCACTC
GGGCGCTTCCAAAGGCTTCTCCAAACCCCTTAAAGACCGCGAGAAAGCTCCCGAGCTCTTCTCCCACTC
80 90 100 110 120 130 140
AGGATCGAGTTGGAGAGGAATTCAGCCATCAGAAAGTACTGTGGCCCTTGAACGGGCCACTGAGCC
AGGATCGAGTTGGAGAGGAATTCAGCCATCAGAAAGTACTGTGGCCCTTGAACGGGCCACTGAGCC
150 160 170 180 190 200 210
AGAACTCAAGCTCAGCGAGAGCCCAAGTGAAGATGTTGTTCCAGAACAGACCTCTTAAAGCTAAGCGAAAGC
AGAACTCAAGCTCAGCGAGAGCCCAAGTGAAGATGTTGTTCCAGAACAGACCTCTTAAAGCTAAGCGAAAGC
220 230 240 250 260 270 280
AGAACTCAAGCTCAGCGAGAGCCCAAGTGAAGATGTTGTTCCAGAACAGACCTCTTAAAGCTAAGCGAAAGC
AGAACTCAAGCTCAGCGAGAGCCCAAGTGAAGATGTTGTTCCAGAACAGACCTCTTAAAGCTAAGCGAAAGC
290 300 310 320 330 340 350 360
AGTCTCCTCGAGCTGGAGAGCTTGAAGAACCTCTTGGCGGCGCTTGAAGAGAGGCGCTTCTCC
AGTCTCCTCGAGCTGGAGAGCTTGAAGAACCTCTTGGCGGCGCTTGAAGAGAGGCGCTTCTCC
370 380 390 400 410 420 430
GGGCGCTCCTCGGCTTCCGTTAAACACTATCTTACCACTACCTGTGACGCGGAGCTGAGACC
GGGCGCTCCTCGGCTTCCGTTAAACACTATCTTACCACTACCTGTGAGCTGAGAGCTGAGACC
440 450 460 470 480 490 500
CAGCTTTTGTGAATGCGAGCTCAGGTACCAACCATATGATCAAAATGCGCTTCCAGAGGCTCTAT
CAGCTTTTGTGAATGCGAGCTCAGGTACCAACCATATGATCAAAATGCGCTTCCAGAGGCTCTAT
510 520 530 540 550 560 570
GAAAGCAGCAAGGGGCGAAGTCAAGGAGCAAGGGGTGACACCCAAAGCTATTTGAGATTGGAGTTGGAGAA
GAAAGCAGCAAGGGGCGAAGTCAAGGAGCAAGGGGTGACACCCAAAGCTATTTGAGATTGGAGTTGGAGAA
580 590 600 610 620 630 640
TCTCASAATCTTCACTGAGTGAACAATGAACAACAAGACAGTGAAGTTTAAATACCTAAGTATTTCCC
TCTCASAATCTTCACTGAGTGAACAATGAACAACAAGACAGTGAAGTTTAAATACCTAAGTATTTCCC
650 660 670 680 690 700 710 720
CAGTGATACCTAGGCTATTTTGTGCTTGGGCTACCTGTTTAAAGGGAGAGAGGAAATCAAGTGG
CAGTGATACCTAGGCTATTTTGTGCTTGGGCTACCTGTTTAAAGGGAGAGAGGAAATCAAGTGG
730 740 750 760 770 780 790
TATTTTCAGCACTTGTATGATTTTGAATGAGCTTAAACCAAGAGATTCGTTCTGCACTCATCTCC
TATTTTCAGCACTTGTATGATTTTGAATGAGCTTAAACCAAGAGATTCGTTCTGCACTCATCTCC
800 810 820 830 840 850 860
TATTTTCAGCACTTGTATGATTTTGAATGAGCTTAAACCAAGAGATTCGTTCTGCACTCATCTCC
TATTTTCAGCACTTGTATGATTTTGAATGAGCTTAAACCAAGAGATTCGTTCTGCACTCATCTCC

[illegible]

[illegible]

[illegible]

2640 2650 2660 2670 2680 2690 2700 2710
 TGTGATCCATCTGCTTTTCCCATTTGAACTATGATTAACCATCTCTGTAAGTGAAGAAACATCT
 TGTGAATCCATCTGCTTTTCCCATTTGAACTATGATTAACCATCTCTGTAAGTGAAGAAACATCT
 170 180 190 200 210 220 230
 2720 2730 2740 2750 2760 2770 2780
 GAAGAGTACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTC
 GAAGAGTACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTC
 240 250 260 270 280 290 300
 2790 2800 2810 2820 2830 2840 2850
 TTCTATCCGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 TTCTATCCGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 310 320 330 340 350 360 370 380
 2860 2870 2880 2890 2900 2910 2920
 AAGTCTGATCTGAACTTAACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAG
 AAGTCTGATCTGAACTTAACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAG
 390 400 410 420 430 440 450
 2930 2940 2950 2960 2970 2980
 AGTCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 AGTCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 460 470 480 X

5. US-09-439-313-335 (1-2984)
 US-09-352-616A-4 Sequence 453, Application US/09352616A

Sequence 453, Application US/09352616A
 Patent No. 6395278
 GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C.
 APPLICANT: Harlocker, Susan Louise
 APPLICANT: Jiang, Yuqi
 APPLICANT: Xu, Jiangchun
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 FILE REFERENCE: 210121.427C8
 CURRENT APPLICATION NUMBER: US/09/352.616A
 CURRENT FILING DATE: 1999-07-13
 NUMBER OF SEQ ID NOS: 472
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 453
 LENGTH: 317
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)...(317)
 OTHER INFORMATION: n = A,T,C or G

Initial Score = 310 Optimized Score = 311 Significance = 2.34
 Residue Identity = 98% Matches = 311 Mismatches = 6
 Gaps = 0 Conservative Substitutions = 0

2600 2610 2620 2630 2640 2650 2660
 TTGCAAAAAAAGTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 TACATCTGCTTTTCCCATTT
 .X
 10 20
 2670 2680 2690 2700 2710 2720 2730
 GGAAGTACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAG
 GGAAGTACTGATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAGCATTCAG
 30 40 50 60 70 80 90

2740 2750 2760 2770 2780 2790 2800 2810
 GTGAATGATGCTTCAACACCATTTTCCAGACAGCTGTTCTATCCGTTTAAATTAATTAATTAAT
 GTGAATGATGCTTCAACACCATTTTCCAGACAGCTGTTCTATCCGTTTAAATTAATTAATTAAT
 100 110 120 130 140 150 160
 2820 2830 2840 2850 2860 2870 2880
 GTTCTACATGATTAACAAACCTGCTCAATCTGTCACATTAAGTGTGATTTGAAGTTAGTACGA
 GTTCTACATGATTAACAAACCTGCTCAATCTGTCACATTAAGTGTGATTTGAAGTTAGTACGA
 170 180 190 200 210 220 230
 2890 2900 2910 2920 2930 2940 2950
 CCCCACCAAACTTTTCTGATGCTTTTTCGACATATGAGTGTGTTGAAAATTAAGTACCATGTC
 CCCCACCAAACTTTTCTGATGCTTTTTCGACATATGAGTGTGTTGAAAATTAAGTACCATGTC
 240 250 260 270 280 290 300 310
 2960 2970 2980
 TTATTAAGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 TTATTA
 X

6. US-09-439-313-335 (1-2984)
 US-09-020-956-11 Sequence 115, Application US/09020956

Sequence 115, Application US/09020956
 Patent No. 6261562
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSER: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/020.956
 FILING DATE: 09-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-6031
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 115
 SEQUENCE CHARACTERISTICS:
 LENGTH: 366 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens

Initial Score = 278 Optimized Score = 364 Significance = 2.06
 Residue Identity = 99% Matches = 365 Mismatches = 1
 Gaps = 2 Conservative Substitutions = 0

TELEFAX: (206) 682-6031

SOE I WAKE: F
SEO ID NO 115

LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.06
Residue Identity = 99% Matches = 365 Mismatches = 1
Gaps = 2 Conservative Substitutions = 0

```
2470 2480 2490 2500 2510 2520 2530
TCTTACATTTCTTTAAATAAGCATTTAGTGTCTGCTCCTAGTCCCTAGTACGAGTACTCTTCTCTCCCTCTCTG
|||||
GCTCTTCTCTCCCTCTCTG
X
10 20

2540 2550 2560 2570 2580 2590 2600
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
30 40 50 60 70 80 90

2610 2620 2630 2640 2650 2660 2670
AAAAAAGTGTCTTTGTTTAAATTAATCTGTGTGTAATCCATCTGTTTCTCCCATTTGAACTAGTC
|||||
AAAAAAGTGTCTTTGTTTAAATTAATCTGTGTGTAATCCATCTGTTTCTCCCATTTGAACTAGTC
100 110 120 130 140 150 160

2680 2690 2700 2710 2720 2730 2740
ATTACCCATCTCTGAACTGTGTGAGAAAAACATCTGAGAGCTAGTCTATCAGAGATGACAGTGAATTGGA
|||||
ATTACCCATCTCTGAACTGTGTGAGAAAAACATCTGAGAGCTAGTCTATCAGAGATGACAGTGAATTGGA
170 180 190 200 210 220 230

2750 2760 2770 2780 2790 2800 2810 2820
TGTTCTCAGAACCATTTGACCCAGACAGCTTCTTCTATCTGTTTAAATTAATGTTGGTCTCTACA
|||||
TGTTCTCAGAACCATTTGACCCAGACAGCTTCTTCTATCTGTTTAAATTAATGTTGGTCTCTACA
240 250 260 270 280 290 300

2830 2840 2850 2860 2870 2880 2890
TGCATTAACAACCCCTGCTCAATCTGTACATTAAGTCTGTGACTTGAAGTTAGTCAGACCCACCAAA
|||||
TGCATTAACAACCCCTGCTCAATCTGTACATTAAGTCTGTGACTTGAAGTTAGTCAGACCCACCAAA
310 320 330 340 350 360 X

ACTTATATTTTCTATGTGTGTTTGTGCAACATATGAG
2900 2910 2920
```

9. US-09-439-313-335 (1-2984)

US-09-232-149A-1 Sequence 115, Application US/09232149A

Sequence 115, Application US/09232149A
Patent No. 6465611
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
FILE REFERENCE: 210121.4276
CURRENT APPLICATION NUMBER: US/09/232.149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.06
Residue Identity = 99% Matches = 365 Mismatches = 1
Gaps = 2 Conservative Substitutions = 0

```
2470 2480 2490 2500 2510 2520 2530
TCTTACATTTCTTTAAATAAGCATTTAGTGTCTGCTCCTAGTCCCTAGTACGAGTACTCTTCTCTCCCTCTCTG
|||||
GCTCTTCTCTCCCTCTCTG
X
10 20

2540 2550 2560 2570 2580 2590 2600
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
30 40 50 60 70 80 90

2610 2620 2630 2640 2650 2660 2670
AAAAAAGTGTCTTTGTTTAAATTAATCTGTGTGTAATCCATCTGTTTCTCCCATTTGAACTAGTC
|||||
AAAAAAGTGTCTTTGTTTAAATTAATCTGTGTGTAATCCATCTGTTTCTCCCATTTGAACTAGTC
100 110 120 130 140 150 160

2680 2690 2700 2710 2720 2730 2740
ATTACCCATCTCTGAACTGTGTGAGAAAAACATCTGAGAGCTAGTCTATCAGAGATGACAGTGAATTGGA
|||||
ATTACCCATCTCTGAACTGTGTGAGAAAAACATCTGAGAGCTAGTCTATCAGAGATGACAGTGAATTGGA
170 180 190 200 210 220 230

2750 2760 2770 2780 2790 2800 2810 2820
TGTTCTCAGAACCATTTGACCCAGACAGCTTCTTCTATCTGTTTAAATTAATGTTGGTCTCTACA
|||||
TGTTCTCAGAACCATTTGACCCAGACAGCTTCTTCTATCTGTTTAAATTAATGTTGGTCTCTACA
240 250 260 270 280 290 300

2830 2840 2850 2860 2870 2880 2890
TGCATTAACAACCCCTGCTCAATCTGTACATTAAGTCTGTGACTTGAAGTTAGTCAGACCCACCAAA
|||||
TGCATTAACAACCCCTGCTCAATCTGTACATTAAGTCTGTGACTTGAAGTTAGTCAGACCCACCAAA
310 320 330 340 350 360 X

ACTTATATTTTCTATGTGTGTTTGTGCAACATATGAG
2900 2910 2920
```

10. US-09-439-313-335 (1-2984)

US-09-159-812-11 Sequence 115, Application US/09159812A

Sequence 115, Application US/09159812A
Patent No. 6413872
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
FILE REFERENCE: 210121.4285
CURRENT APPLICATION NUMBER: US/09/159.812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 366
TYPE: DNA
ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.06
Residue Identity = 99% Matches = 365 Mismatches = 1
Gaps = 2 Conservative Substitutions = 0

```
2470 2480 2490 2500 2510 2520 2530
TCTTACATTTCTTTAAATAAGCATTTAGTGTCTGCTCCTAGTACGAGTACTCTTCTCTCCCTCTCTG
|||||
GCTCTTCTCTCCCTCTCTG
X
10 20

2540 2550 2560 2570 2580 2590 2600
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
|||||
AATTAAATCTTTCACTTGCATTTGCAAGAGATTACACATTTGCTGTGATGATATGTTGCAAAAA
290 300 310 320 330 340 350 360
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240 250 260 270 280 290 300
TGCATACAAACCTGCTCATCTGTCATCAATTAAGTGTGATGATTAAGTACAGACCCCAACCA
TGATACAAACCTGCTCATCTGTCATCAATTAAGTGTGATGATTAAGTACAGACCCCAACCA
310 320 330 340 350 360 X
2900 2910 2920
ACTTATTTTCTATGATGTTTTCACATATGAG

13. US-09-439-313-335 (1-2984)

US-09-030-607-20 Sequence 207, Application US/09030607

Sequence 207, Application US/09030607

Patent No. 6262245

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: DILLON, DAVIN C.

NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESSES:

ADDRESS: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

Initial Score = 253 Optimized Score = 318 Significance = 1.84

Residue Identity = 96% Matches = 322 Mismatches = 7

Gaps = 4 Conservative Substitutions = 0

CCCAAGCTTATCTGCTTGAATTTTAAAAAGTTGGGGGAGATTTGTAATTTGCTTAAAGATGCA

1550 1560 1570 1580 1590 X 1600 1610

TTTAAACCTGACCTCTTATTTCTTCTTAAATAATATGATTAATCCCAATCTTATTTAAAG

1620 1630 1640 1650 1660 1670 1680

TTTTTAAACCTGACCTCTTATTTCTTCTTAAATAATATGATTAATCCCAATCTTATTTAAAG

1690 1700 1710 1720 1730 1740 1750

ACCTGACCTGAGAGGTGACCTGATGATTAAGACCTTCTGAGTGTCTGCTGTTAGCTTGAAGTC

ACCTGACCTGAGAGGTGACCTGATGATTAAGACCTTCTGAGTGTCTGCTGTTAGCTTGAAGTC

100 110 120 130 140 150 160

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

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170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230

TGACATCTCTGAGAAATCTTGTGATGAGAGAGGATGAGATTTGATTTTCACAGAGAGAAACACAGC

1760 1770 1780 1790 1800 1810 1820 1830
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 170 180 190 200 210 220 230
 1840 1850 1860 1870 1880 1890
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG
 240 250 260 270 280 290 300
 1900 1910 1920 X 1930 1940 1950 1960 1970
 CAGCTTAGGCCCCGGGGAGGCCCACTGACAGCAAGAGGACTGAGCCTTTTGCAGAAAGAGCT
 CAGCTTAGGCCCCGGGGAGGCCCA
 310 320 330 X

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15. US-09-439-313-335 (1-2984)
 US-09-232-149A-2 Sequence 207, Application US/09232149A

Sequence 207, Application US/09232149A
 Patent No. 6465611
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 FILE REFERENCE: 210121.427C6
 CURRENT APPLICATION NUMBER: US/09/232.149A
 CURRENT FILING DATE: 1999-01-15
 NUMBER OF SEQ ID NOS: 338
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 207
 LENGTH: 332
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(332)
 OTHER INFORMATION: n = A,T,C or G
 Initial Score = 253 Optimized Score = 318 Significance = 1.84
 Residue Identity = 96% Matches = 322 Mismatches = 7
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610
 CCCAAGCTTATCTGCTTGAATTTTAAAAAGTTGGGGCAGATTCTGAATTTGGCTAAAGACATGCA
 TGAATTTGGCTAAAGAC-TGCA
 X 10 20
 1620 1630 1640 1650 1660 1670 1680
 TTTTAAAGCTTGAAGATCTTTCATGACAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 TTTTAAAGCTTGAAGATCTTTCATGACAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 30 40 50 60 70 80 90
 1690 1700 1710 1720 1730 1740 1750
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 100 110 120 130 140 150 160
 ACTTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 1760 1770 1780 1790 1800 1810 1820 1830
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC

170 180 190 200 210 220 230
 1840 1850 1860 1870 1880 1890
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG
 240 250 260 270 280 290 300
 1900 1910 1920 X 1930 1940 1950 1960 1970
 CAGCTTAGGCCCCGGGGAGGCCCACTGACAGCAAGAGGACTGAGCCTTTTGCAGAAAGAGCT
 CAGCTTAGGCCCCGGGGAGGCCCA
 310 320 330 X

A

16. US-09-439-313-335 (1-2984)
 US-09-159-812-20 Sequence 207, Application US/09159812A

Sequence 207, Application US/09159812A
 Patent No. 6613872
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
 FILE REFERENCE: 210121.428C5
 CURRENT APPLICATION NUMBER: US/09/159.812A
 CURRENT FILING DATE: 1998-09-23
 NUMBER OF SEQ ID NOS: 306
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 207
 LENGTH: 332
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(332)
 OTHER INFORMATION: n = A,T,C or G
 Initial Score = 253 Optimized Score = 318 Significance = 1.84
 Residue Identity = 96% Matches = 322 Mismatches = 7
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610
 CCCAAGCTTATCTGCTTGAATTTTAAAAAGTTGGGGCAGATTCTGAATTTGGCTAAAGACATGCA
 TGAATTTGGCTAAAGAC-TGCA
 X 10 20
 1620 1630 1640 1650 1660 1670 1680
 TTTTAAAGCTTGAAGATCTTTCATGACAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 TTTTAAAGCTTGAAGATCTTTCATGACAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 30 40 50 60 70 80 90
 1690 1700 1710 1720 1730 1740 1750
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 100 110 120 130 140 150 160
 ACTTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTTCGCTGCTTCTGCTTGAAGT
 1760 1770 1780 1790 1800 1810 1820 1830
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGAGAAACACAGC
 170 180 190 200 210 220 230
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGGAGGCTCATGGTGGACATGAAAGAGG

GCAGAAATGAGGGCCAGCTTACTAGCTTGTCCACTGAGGGCTCATGGTGGAGCATGAGAAAGAGG
240 250 260 270 280 290 300
1900 CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT
1910 1920 X 1930 1940 1950 1960 1970
CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT
310 320 330 X

A

17. US-09-439-313-335 (1-2984)

US-09-115-453-20 Sequence 207, Application US/09115453B

Sequence 207, Application US/09115453B
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115.453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(332)
OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84
Residue Identity = 96% Matches = 322 Mismatches = 7
Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610
CCCAAGCTTATCTGTCTTGACTTTTAAAAAGTTGGGGCAGATCTGAATTTGGCTAAAGACATGCA
TGAATTTGGCTAAAGAC-TGCA X 10 20

1620 1630 1640 1650 1660 1670 1680
TTTTTAAACTAGCACTTATTTCTTTCTTTTAAATAATACATAGCATTAATCCCAATCCTATTAAAG
TTTTTAAACTAGCACTTATTTCTTTCTTTTAAATAATACATAGCATTAATCCCAATCCTATTAAAG
30 40 50 60 70 80 90

1690 1700 1710 1720 1730 1740 1750
ACCTGACAGCTTGAAGAGTCACTACTGATTAAGACCTTCTGGTGTCTGCTTTAGCTTTGAAGTC
ACCTGACAGCTTGAAGAGTCACTACTGATTAAGACCTTCTGGTGTCTGCTTTAGCTTTGAAGTC
100 110 120 130 140 150 160

1760 1770 1780 1790 1800 1810 1820 1830
TGACATCTCTTGAATCTTTGATGACAGAGGATTAAGAGCTTATTTTCAAGAGAAACACACAC
TGACATCTCTTGAATCTTTGATGACAGAGGATTAAGAGCTTATTTTCAAGAGAAACACACAC
170 180 190 200 210 220 230

1840 1850 1860 1870 1880 1890 1900
GCAG-AATGAA-GGGCAGAGCTTACTGAGC-TGTCCAGTGAAGGGGCTCATGGTGGGACATGGAAGAGG
GCAG-AATGAA-GGGCAGAGCTTACTGAGC-TGTCCAGTGAAGGGGCTCATGGTGGGACATGGAAGAGG
240 250 260 270 280 290 300

1910 1920 X 1930 1940 1950 1960 1970
CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT
CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT

CAGCTTAGGCCCCGGGGAGCCCA
310 320 330 X

A

18. US-09-439-313-335 (1-2984)

US-09-288-946-20 Sequence 207, Application US/09288946

Sequence 207, Application US/09288946
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C7
CURRENT APPLICATION NUMBER: US/09/288,946
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 207
LENGTH: 332
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(332)
OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84
Residue Identity = 96% Matches = 322 Mismatches = 7
Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610
CCCAAGCTTATCTGTCTTGACTTTTAAAAAGTTGGGGCAGATCTGAATTTGGCTAAAGACATGCA
TGAATTTGGCTAAAGAC-TGCA X 10 20

1620 1630 1640 1650 1660 1670 1680
TTTTTAAACTAGCACTTATTTCTTTCTTTTAAATAATACATAGCATTAATCCCAATCCTATTAAAG
TTTTTAAACTAGCACTTATTTCTTTCTTTTAAATAATACATAGCATTAATCCCAATCCTATTAAAG
30 40 50 60 70 80 90

1690 1700 1710 1720 1730 1740 1750
ACCTGACAGCTTGAAGAGTCACTACTGATTAAGACCTTCTGGTGTCTGCTTTAGCTTTGAAGTC
ACCTGACAGCTTGAAGAGTCACTACTGATTAAGACCTTCTGGTGTCTGCTTTAGCTTTGAAGTC
100 110 120 130 140 150 160

1760 1770 1780 1790 1800 1810 1820 1830
TGACATCTCTTGAATCTTTGATGACAGAGGATTAAGAGCTTATTTTCAAGAGAAACACACAC
TGACATCTCTTGAATCTTTGATGACAGAGGATTAAGAGCTTATTTTCAAGAGAAACACACAC
170 180 190 200 210 220 230

1840 1850 1860 1870 1880 1890 1900
GCAG-AATGAA-GGGCAGAGCTTACTGAGC-TGTCCAGTGAAGGGGCTCATGGTGGGACATGGAAGAGG
GCAG-AATGAA-GGGCAGAGCTTACTGAGC-TGTCCAGTGAAGGGGCTCATGGTGGGACATGGAAGAGG
240 250 260 270 280 290 300

1910 1920 X 1930 1940 1950 1960 1970
CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT
CAGCTTAGGCCCCGGGGAGCCCATGCTGAGCAAGGAGGAGTGTGAGGCTTTTCAGAGAAAGGCT
310 320 330 X

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19. US-09-439-313-335 (1-2984)
US-09-352-616A-2 Sequence 295, Application US/09352616A

Sequence 295, Application US/09352616A
Patent No. 6395278

APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi

APPLICANT: Xu, Jiangchun
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.427C8

Initial Score	=	215	Optimized Score	=	303	Significance	=	1.50
Residue Identity	=	98%	Matches	=	305	Mismatches	=	0
Gaps	=	4	Conservative Substitutions	=			=	0

[illegible][illegible]

2610 2620 2630 2640 2650 2660 2670
 AAAAAAAAAAGCGCTGTTAAATACTGGTTGATCCATCGTTTTCCTGATGACCTG
 AAAAAAAAAAGTGTCTGTTAAATACTGGTTGATCCATCGTTTTCCTGATGACCTG
 AAAAAAAAAAGTGTCTGTTAAATACTGGTTGATCCATCGTTTTCCTGATGACCTG
 100 110 120 130 140 150 160

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[illegible]

2820 2830 2840 2850 2860
CATGATAACAACCGCTGCCAATCTGTACATAAAGTCTGTGACTT

20. US-09-439-313-335 (1-2984)
US-09-232-149A-2 Sequence 295, Application US/09232149A

Sequence 295, Application US/09232149A
Patent No. 6465611

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer Lynn
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
 PTE REFERENCE: 310131 40705

FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ. ID NOS. 338

Initial Score	=	215	Optimized Score	=	303	Significance	=	1.50
Residue Identity	=	98%	Matches	=	305	Mismatches	=	0
Gaps	=	4	Conservative Substitutions				=	0

[illegible]

2540	2550	2560	2570	2580	2590	2600
TGAATTTAATCTTCACTGCAATTTGCAGAGATTACACATTCACGTGATGATATTTGTGGAAAA						
TGAATTTAATCTTCACTGCAATTTGCAGAGATTACACATTCACGTGATGATATTTGTGGAAAA						
TGAATTTAATCTTCACTGCAATTTGCAGAGATTACACATTCACGTGATGATATTTGTGG----						
30	40	50	60	70	80	90

2610 2620 2630 2640 2650 2660 2670
 AAAAAAAAAAGTCTTGTGTTAAATTAAGTTGGATGATCATCTGTCTTTTCCCATTTGAACTAG
 AAAAAAAAAAGTCTTGTGTTAAATTAAGTTGGATGATCATCTGTCTTTTCCCATTTGAACTAG
 AAAAAAAAAAGTCTTGTGTTAAATTAAGTTGGATGATCATCTGTCTTTTCCCATTTGAACTAG
 100 110 120 130 140 150 160

2660 2590 2700 2710 2720 2730 2740
TCATTAAACCCATCTCTCAACTGTGAGAAAAACATCTGAAGAAGTGTCTATCAGATCTGCACAGCTGAATTG
TCATTAAACCCATCTCTCAACTGTGAGAAAAACATCTGAAGAAGTGTCTATCAGATCTGCACAGCTGAATTG
TCATTAAACCCATCTCTCAACTGTGAGAAAAACATCTGAAGAAGTGTCTATCAGATCTGCACAGCTGAATTG

[illegible]

2820 2830 2840 2850 2860
CATGCATACAAACCCCTGCTCCAATCTGTACATAAAGTCTGTGACTT

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The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Frame
1. US-09-105-470B-8	Sequence 8, Application U	3488	50	556
2. US-09-105-470B-2	Sequence 25, Application	3974	44	830
3. US-09-105-470B-2	Sequence 27, Application	415	43	182
4. US-09-105-470B-3	Sequence 3, Application U	705	42	308
5. US-09-105-470B-1	Sequence 1, Application U	705	42	308
6. US-09-105-470B-2	Sequence 29, Application	533	34	229
7. US-09-105-470B-3	Sequence 30, Application	318	33	152
8. US-09-105-470B-2	Sequence 26, Application	112	28	54
9. US-09-105-470B-2	Sequence 28, Application	507	25	219
10. US-09-105-470B-1	Sequence 16, Application	26	12	14
11. US-09-105-470B-2	Sequence 20, Application	24	11	13
12. US-09-105-470B-1	Sequence 15, Application	27	11	13
13. US-09-105-470B-2	Sequence 24, Application	19	10	13
14. US-09-105-470B-2	Sequence 22, Application	15	9	10
15. US-09-105-470B-1	Sequence 19, Application	26	9	15
16. US-09-105-470B-1	Sequence 18, Application	28	9	15
17. US-09-105-470B-1	Sequence 17, Application	26	9	13
18. US-09-105-470B-2	Sequence 21, Application	15	8	8
19. US-09-105-470B-2	Sequence 21, Application	24	8	13
1. US-09-700-700-1 (1-1936)	Application US/09105470B			
US-09-105-470B-8	Sequence 8, Application US/09105470B			
Initial Score = 50	Optimized Score = 556	Significance = 1.74		
Residue Identity = 47%	Matches = 678	Mismatches = 567		
Gaps = 167	Conservative Substitutions = 0			
TCCTCCGGTGTCCAGGAGAGAGAGTCCACTTATTTCTTCTCCGTGACCTTCGATGATGAGCGACCGAACGCC				
2100 2110 2120 2130 2140 X 2150 2160				
T-TTACAGCGTGCGCCCAATAAGAA--CAAG-ANG-CACTGCGTGATTTTAAACAACAAGCTGTATTAACAAGA				
TCGTATTAGCGAAGAGGAATTAAGCCCAAGAGAGCTGCTGTGCTT-----CAAGGACACA---AGC				
2170 2180 2190 2200 2210 2220				
90 100 110 120 130 140 150				
ACTCCACTGCAAGAGAGGAGCGCGCGG-CAGGA-GAATCTCCCGTGTCCCAAGACAGGGGCTT--AAGGAGG				
CCCTCTCTG-CCACTCGAATCTTAACACCGAGTCTTTTGGTGTGCGCTTCCCGGATCTTGTTCACAG				
2230 2240 2250 2260 2270 2280 2290 2300				
160 170 180 190 200 210 220				
GTGTCCACACTGCTGCTGAGGGCGGTGATTTTATTTATTAAGAAAG--TGAAAGGCGCTTCTCA-ACT				
GCAATTTCCCTGC-CT---CCCT-CTCCGCTCTCTCTCAGACACAGATCCAGAAATCCCAATATATTTCT				
2310 2320 2330 2340 2350 2360				
230 240 250 260 270 280 290				
TTTTTCCCTGGGCTGAGAAATTTAGATCA-GAA--GTTTC---CT-GGAGTT--TTACAGGCTATCATATAT				
ACTTAGACAGTAG--GGAGAAAGTTCAACACACAGACAGTCTTAACCTTTGGGCTTGTAGAT-TCTTACGA				
2370 2380 2390 2400 2410 2420 2430				
300 310 320 330 340 350				
ACTGATACCTCGAAGAGCAATATATTTCTT---CTTCCCGCTTTTAAATTTTGGTGTCTTTTGCA---				
AATGAAGCGTAA--TAAACATATTTTACTACTCTACTCC--GGAGACTCTTATGATGATGAAAAG				
2440 2450 2460 2470 2480 2490 2500				
360 370 380 390 400 410				
-GCAAT-TACTCAC--TAAAG--GGC--TTCAAT---TTAGTCCAGATTTTAAAGTGTGCGTCACTCACTACT				
TGAATATATCCACGATGACAGGCGGTGTTGTTTACTACTACTCAATAAAG--CATAAAGGTGATGATTTCTCT				

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2510      2520      2530      2540      2550      2560      2570
420      430      440      450      460      470      480
TATGCGCTGTTATTAAGCCG-AGATCTGCTT-TTTTGTGTTTTTTTTTTCGCTCCCAAG-
TCT-CTTCCCT-GCTAACGTGTAATCTTGTCTCCATCCCTCCCTCCCACTCC-TTTCCAGAAAG
2580      2590      2600      2610      2620      2630      2640
--CT-----TATCGTCTGATCTTTTAAAGTTGGGGGAGATTC-TGATTTGGCTAAAGACA
CATTTGGGCTTATTTGT-TGAC-TCTGAAACACTTCAGCGCCCTCCCAAGGCTCCCAACCCCTA
2650      2660      2670      2680      2690      2700      2710
550      560      570      580      590      600      610
TGCAATTTTAAACAGAGCACTTCTTATTTCTTCCTTAAATATACATTAATCCCAAT---CC
AGCAGCCGAGAGAGCGCTCCGAGCTGCTTC-TCCACACTCAGGTGATGAGTGAAGAGATTCACG
2720      2730      2740      2750      2760      2770      2780
620      630      640      650      660      670      680
TATTTAAG-ACCTGACAGCTTGAGAA-GGTCACTACTG--CATTTATAGACCTTCTGTGCTTC---TG
CATCAAGTATCTGTGCGCCCTCCCTGAGCGGCCACCTGCGCAAGACCTCAAGCTCAAGAGACCCAGTG
2790      2800      2810      2820      2830      2840      2850
690      700      710      720      730      740      750
CTGTACGTTTGAAG-TCTGACATCTCTGAGATCTTTGATGATGAGAGAGATTAATTTGATTTTC
AGATATGCTTCCAGAACAGAC--GCTATTAAGCTAACGAAAGAGCTCTCTCTGGAG--CTGGAGACTT
2860      2870      2880      2890      2900      2910      2920
760      770      780      790      800      810      820
ACAGGAGAAAGACACAGCGCAG--AATGAGGCGCAGGCTTACT---GAGGCT-----GTC-CAGTG---GA
GAGAGAGACTCTCTTTGGCCGCGCTGAAAGAGAGAGGCTTCTCCGCGCTCTCTGCTCGGTATTA
2930      2940      2950      2960      2970      2980      2990
810      820      830      840      850      860      870
GGGCTCATGGGTGGACATGAGAAAGAGAGCGAGCTAGGC-CTGGGAGGCGCGATGCTGACAGCA--GCA
CAGCT-ATCTTACTACCATTAACCTGTA--CTGGGTGGAGGAGCT--GGAAGCCAG--CTTTGGGTATGCA
3000      3010      3020      3030      3040      3050      3060
880      890      900      910      920      930      940
GGGACTGATGAGCTTTTGGAGAAA--GGCTAAGAAAAGAAAACCATTTAAACACA-----CAA
GCTCAGGTGACACATTAATGATCAAAAAGCTCTCCCAAGGCTGCTTAAGAAAGACAAAGGGGCA
3070      3080      3090      3100      3110      3120      3130
950      960      970      980      990      1000      1010
-GAAACTGTCCAATGCTTTGGAACTGTGTTATGCTATATAGGTCCCAAAATGGGTAACTAGACT
GTCAGGAGCAAGAGGTGTCACACCAAGCTATGAGAT-TTGGGT-GGAATCTCAG-ATTCTTACT
3140      3150      3160      3170      3180      3190      3200
1020      1030      1040      1050      1060      1070      1080
TCAGAGGAGT---AGCAGAG--GCAAGAGAAAT-CT--GGCTGCTCTTCAATTTTCAATTTCTGTT
GTTGAGCAATGAAACAAGAGAGAGAGTAAAGTTTAACTTAAGTATTC-TCCA-GTGCATACG-T
3210      3220      3230      3240      3250      3260      3270
1080      1090      1100      1110      1120      1130      1140
ATCTCAGGAGCTGTGAGGAGAGACATTAAGAAAATGAAACAACAACAATTACTA--ATGAGTA
AGGTCAATTTTGTGCTGCTACCTGTTTGAAGGGA-GAGAGGAAATCAAGTGTATTTTTCAGCA
3280      3290      3300      3310      3320      3330      3340
1150      1160      1170      1180      1190      1200      1210
CGGTG-AGGCTGGAGCTCTTGACTCACTAATTTCCGTTAGTGAAGAACTTTCAATTTCTTTT
CTTTGATATTTTGTATGATG-TTGAACCAAGAGATTCGTT--ATGCAATCCCATTC--TCTGTGTC
3350      3360      3370      3380      3390      3400

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1220      1230      1240      1250      1260      1270      1280
ATTGGAAGGCGACCTTACTGTTGTGCGAAATTTGCCAATTAATTAATGAAGTTGGCAATTTAC
ACT-GAA-TATCACT-CTG-----AAGAGCAAACTTA--CAGAGAAA--GACAA-----
3410      3420      3430      3440      3450
1290      1300      1310      1320      1330      1340      1350      1360
CCATTTCTGTGTTTGGGCTCCACATGTCATGTCATGTCACAGTCTGCTGACACCGAGAGTACTA
CCA--GGATAGAT--GTACACA-ACTG-AAT-TAACTC
3460      3470      3480      3490      3500      3510      3520
GCCAGCACAAGAGCAGGGT
1370      1380      1390      1400      1410      1420
ATTTTCCCATGAGAGCGTACGCGACTGGCGGTGAGAGATCTGTGTCGATTTGGTCCAGCAATTCGG
1740      1750      1760      1770      1780      1790      1800
30      40      50      60      70      80      90
TTTACAGGTGCGCCCAATTAAGAAAGATGCACTGCTGTGATTTAAGACAACT-GTATTAACA--GAAC
CTGTAGCG-GGCCCATTAAGTCTGTGTCGCGCG--TCTGCTCT--GGCTGCTGCAATTAATCTGAC
1810      1820      1830      1840      1850      1860      1870
100      110      120      130      140      150      160
TC-CACTGCA-----GAGGAGGCGCG--GCCA--GAG--AATCTCGCTGTGTC--CAAGACAG
TGCATCAAAATTCAGCCGATGAGGGAACGGAAGCGAGCTGATGTCATGTCGCTTTTCAACAACAT
1880      1890      1900      1910      1920      1930      1940
150      160      170      180      190      200      210
G-----GGCTAAGAGGCTCTCCACACTGCTCTAGGAGCT-GTTCATTTTATTAAGAAAGTGA
GCAATGCTGAATGAGGAGCTGTTCCACATGC--GATGCTGTGTCACAGATGAGCGCTGAGCGCA
1950      1960      1970      1980      1990      2000      2010
220      230      240      250      260      270      280
AGGC-CTC--TTTCAA--CTTTTCCC-TTGGGCTGAGAAAT--TA--GAATCAGAGTTTCTGTC
AATGGCGCATTAACGAGTCGGGCTCGGTTGGTGGATATCTGGTGAAGGATACAGATAC-GA
2020      2030      2040      2050      2060      2070      2080
270      280      290      300      310      320      330
AGTTTCAAGGCTATCATATATATCTGATCTGTAAGGACAATAATTTCTTCCCTCTTTT-----AAA
AG---AAGGCTCATGTTATTCG--CC-GTTAACACATCAAGAGANTTTTCCGCTCTGAGGCAAA
2090      2100      2110      2120      2130      2140      2150
340      350      360      370      380      390      400
AATTTGTGTTCTTTTTCAGCAA-TTACTCA-CTAAGS-GGTTCAATTTAGTCCAGTTTT--TAGCTG
CCACGTGAGAC-GCTTGTGCAACTCTCTCAGGCGCAGCGGTGAAGGCAAT-CAAGTGTGCGCGTCTC
2160      2170      2180      2190      2200      2210      2220
410      420      430      440      450      460      470
GCTGCACTTAATTAAGCC-----TGGCTATTAGC--CCGAGATCGTCTTTTGTGTTTTTTT
ACTGTGAAGAAAGAAACCCCTGCGCCCAATAGAGAAACG-CTCTCCCGCGGTGGCCGATCAT
2230      2240      2250      2260      2270      2280      2290
470      480      490      500      510      520      530

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2. US-09-700-700-1 (1-1936)
 US-09-105-470B-2 Sequence 25, Application US/09105470B

Initial Score = 44 Optimized Score = 830 Significance = 1.35
 Residue Identity = 47% Matches = 1040 Mismatches = 823
 Gaps = 340 Conservative Substitutions = 0

TTTTCCG-TCCTCCCAAGCTTTTATCTGTCTTGAATTTAAAAAGTTGGGGGAGATTCGATTTGGG
 TAATCAGCTGGCAGACAGGTT-----TCCCGAC--TGAAAGGGGAGCTGAGC--GCAACGCAATTAAT
 2300 2310 2320 2330 2340 2350
 540 550 560 570 580 590 600
 CTAAAGA-CATGCAATTTTAA--AACTAGGCAACTCTTATTTCTTCTT-TTAAAAATACATGCAATTA
 2360 2370 2380 2390 2400 2410 2420
 GTAATAGCCGGAATTTGGACCAAGAGCGC--CATCGTCCCTCCCACTCTCGATTCGGGCAATGGA
 610 620 630 640 650 660 670
 ATCCG--AAATCTTAT-TTAAAGACCTGACAGCTTGAAGG--TCACTATCTCATTTATGAGACCTTCTGT
 2430 2440 2450 2460 2470 2480 2490
 TGCGGGAGTAGCCGCTGCTGTTCCTG--GATGCCAGGATTTGACCTCGGTAGAACTCCGCGAGGT
 680 690 700 710 720 730
 GGTTCGTGTACCTTTGAAAGTCTGA--CAA-TC-CTTGAGAAATCTTTGCAATGAGAGAGTTAAGA-----
 2500 2510 2520 2530 2540 2550 2560
 CGTCAGC-CTCA--GGACGACG-CTGAACCACTCGCGAGGGATC--GAGCCCGGGGTG--GCGAAGAACTC
 740 750 760 770 780 790 800
 -GGATTTGATTTTACAGAGAGAAACA--CAGCGCAGATGAAGGGCCAGCTTACTGAGCGTCTCC--
 2570 2580 2590 2600 2610 2620 2630
 CAGCATGATCCCGCGCTGGAGATATCCAGC--CGCGTCCCGGAAAGATTCGCAAGCCCACTTT
 810 820 830 840 850 860
 AGTGAGGGCTCATGATGGTGGACATGAGAA-----AGAAGCAGCTTAGG--CCCTGGGAGGCCAGT--
 2640 2650 2660 2670 2680 2690 2700
 CATAGAAAG--CGGGGGTGG--AATCGAAATCTCGTGAATGGCAGGTGGCGCTCGCTTGTGTGATTTG
 870 880 890 900 910 920
 --CCAATGAG--CAAGC--AAG--GGAC--TGAGTGAAGCTTTTGCAGAGAAAG--CTAAGAAAAAGA--AA
 2710 2720 2730 2740 2750 2760 2770
 AAACCAAGTCCCGCTCGAAGAACTGCTCAAGAGGATGAAGGAGATGCCCTGGATTCGGAGGCGG
 930 940 950 960 970 980 990
 CCATTC--TAAACACACAGAAACTGTC--CAATGCTTTGGGAAGTGTGTTATTTGTC-CTATTAATGGGT
 2780 2790 2800 2810 2820 2830 2840
 CGATTCCTTAAGAC--GAGGAAGGGTCAAGCCATTCGCCGCA--GCTTTCA--GCAATATCAAGGGT
 1000 1010 1020 1030 1040 1050 1060
 CCCCAG--AATGGGTAC--TAGACTTCAGAGATGAGCAGAGAGAGAGAAATCTGGCTGTCTT
 2850 2860 2870 2880 2890 2900 2910
 AGCCACGCTATGT--CCGATAGGGGTCCGCCACCCAGCGGCAAGTCGATGATTCAGAAAAAGCGG
 1070 1080 1090 1100 1110 1120
 CCATTTT-CATTCGTCTTCTAGGTGAGCTGTGA-----GAGGGAGAC--ATTAGA--AAAAATGAACA
 2920 2930 2940 2950 2960 2970 2980
 CCATTTTCCACATATAT-TT-CCGAGCAGAGATTCGCAATGGGTCAAGAGATTCCTCCGCTCGGCA
 1130 1140 1150 1160 1170 1180
 ACAAACAATTAATAGATGATGACCTGAGCGCTGAG--GAGTCTTTGA--CTCCACATCTAAT--TCCG
 2990 3000 3010 3020 3030 3040
 TGCGGGC-CTTGAAGCTGGCGAAGAGTTGG--CTGGCGGAG--CCCTGATCTCTTGTGTCAGATCATTCC-
 1190 1200 1210 1220 1230 1240 1250
 TTTATGAGAA--ACC--TTTCAAT-----TTTCTT--TTATTGAAAGGGCAGACTTACTGTTGGCAAAAT
 3050 3060 3070 3080 3090 3100 3110
 -TGATGCAAAACCGGCTTCATCGAGTATGCTGCTGCTGA--TGGGATGTTTCTGCTTGTGTGAT
 1260 1270 1280 1290 1300 1310
 TGCCA-ACATTAAG--TTAATGAAAGTTG--GCC-AATTTACAC--CCATTTTCTGTGTGTTGGCTCCACA

GGGCGTAGCGGATCAAGGATATGACGCCCGCATGTATGACCATATGATATTT--CTGGGCA
 3120 3130 3140 3150 3160 3170 3180
 1320 1330 1340 1350 1360 1370
 -TTGAATGTTCAATGCCAGTGTGCTGACACG-AC--CG--GAGTACTAGCCAG-----CAGAAAA
 3190 3200 3210 3220 3230 3240 3250
 GGAGCAGGTAGATGACAGAGATCTCGCCCGCATCTGCCCCAATGAGCAGTCCCTCCGCTTCA
 1380 1390 1400 1410 1420 1430
 --GGCAGGT--AGC-CTGAATGTGTTCTCTCTTACAT-TTCTTTAAATTA--AGCAT--TAGTGC
 3260 3270 3280 3290 3300 3310 3320 3330
 GTGACAGCTGAGACAGAGACGCGCAGAGAGCCCGCTGCGCAGCAGAGATAGCCGCCCTGCTGTC
 1440 1450 1460 1470 1480 1490 1500
 T-CAGTCCCTACTAGTACTCTTCTCTCCCTCTCTGAAATTAATTTCTTC-AACTTGCATTTGA--A
 3340 3350 3360 3370 3380 3390 3400
 TGCAATTCATTCAGGGCAC--GGAACAGGTGCTCTTGACAAAAAGAACCGGCGCCCTGC-GCTGACAGCC
 1510 1520 1530 1540 1550 1560
 GGAATAC---ACATTTCA-CTG-TGA-TGTATATGTGTTGCAAGNAAAAAGAGTCTTTGTTAA
 3410 3420 3430 3440 3450 3460 3470
 GGAACACGGCGCATCAGAGACGCGGATGTCTGTGTG--CCAGTCAATCCGAAATGACCTTCACCCAA
 1570 1580 1590 1600 1610 1620 1630
 AATTAATTTG---TTTGTG-AATTCATCTTGTCTTCCCATTTGAAATGATCATTAATCCATCTC-TGA
 3480 3490 3500 3510 3520 3530 3540
 GCGGCGGAGAACCTCGCTGCAATTCATCTTG---TTCAATCAGCAGAAAGCATCTCATCTGCTCTTGA
 1640 1650 1660 1670 1680 1690
 ACTGTGTAAGAAAAATCTG-----AAGA-GCTAGTCTATAGCA--TCTGACAGTGAATGATGATGTTCT
 3550 3560 3570 3580 3590 3600 3610
 TCAGAT-CTTGATCCCTCGGCGCATCAGATCTTGGCGGCAAGAAAGCATTCAGTTTACTTTGAGGGCTT
 1700 1710 1720 1730 1740 1750
 CAGAACCATTTCA-----CCCA--GACA--GCCGTGTTCACTGTGTTTAA-----TTAGTTGG
 3620 3630 3640 3650 3660 3670 3680
 CCAACCTTACAGAGGCGCCCGCAGTGGCAATTCGGTTCGCTGCTCAATAAACGCCAGCT-A
 1760 1770 1780 1790
 GTTCTTACATG-----CATACAAAC--CTGC-TCCATCTG-----TC-----ACATA-
 3690 3700 3710 3720 3730 3740 3750
 GCTATCGCATGTAGAGCCCACTGCAGGCTACTGCTTCTTTGCGGCTGCTGTTTCCCTGTGTCAGATAG
 1800 1810 1820 1830 1840 1850
 -AAAGTCTGTGAC--TTGAAGTTAGTGCAGAC--CCACCCAAATTTATTTTCTATGTTT-----T
 3760 3770 3780 3790 3800 3810 3820
 CCGATGACTGACATTAATTCGGGGTGCAGACCGTTTCTGCGAC--TGGCTTCTACGTTTCCGCTTCT
 1860 1870 1880 1890 1900 1910 1920
 TTGGAACATATAGTGTGTTTGAATAAATAGTACCCATGCTTTATTAATAA--NAAAAAAG--GGC
 3830 3840 3850 3860 3870 3880 3890
 TTAGAGCCCTTGGCCCTGATGCTTCCGCGAC--GTAGAGTTTAAATAACGCAAAAAATATGTTGAC
 1930 X
 --G---GCCGCCGACTAGTA
 3900 3910 X 3920 3930 3940 3950 3960
 TTGAGCGGATTAACAAATTAATGATGATCCCAATGTGAGCGGATTAACATTTCAACATTAAGAGAGAA

Initial Score	=	43	Optimized Score	=	182	Significance	=	1.29
Residue Identity	=	47%	Matches	=	253	Mismatches	=	158
Gaps	=	122	Conservative Substitutions	=	0			

1060	1070	1080	1090	1100	1110	1120	1130
------	------	------	------	------	------	------	------

TTCCATTTTCATCTCTTATCTCAGGTAGCTGAGGAGGAGCATTTGAAAAAATGAAACAACAACAAGC
 1020 1100 1110
 GCTCGAGCT--TTCCACGCA--
 X 10

1140 1150 1160 1170 1180 1190 1200
 AATTACTATGAGTACGCTGAGCCTGGAGTCTTCTGATCTTCACACTTATTATTCGTTTAGTGAAGAAC
 AATCCCAAT-AG--CGTT--GGGTG-CACACTCTTG-CCTCA--CTTG--CC--
 20 30 40 50 60

1210
 TTTCATTTCTTTATTATTAAGGCGCAGCTTACGTGTGGCAAAATTGCCACATAA--GTTAATA-GA
 1220
 TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 1230
 ---CCTGTGCCTTTCARBA---GACACC--CTGGGGAAGGC-AGTTTTCATTAATGATGTCACCT
 70
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 110
 120

1280 1290 1300 1310 1320 1330 1340
 AAGTGGCAATTACCCCATTTCTGTGGTTGGGCTCAATTGAATGTTCAATGCCACGCTGTGTG
 GAGCTGCG-ATT-ACC-AAAAAGCT-----GGGCTTCAC-TGCCACAG-CAGT-ACAGTAGTGGTA
 130 140 150 160 170 180

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ACACCGACCGAGTCTCTAGCCAGACACAAAGCCAGGGTAGCCTTAATTCCTTCTCTTACATTTCTTT
GTAGGATAGCTGTATA-CAGGAGACCAAGAGAGGCCCGGAAAG-GGC---CT-CTCTTT-CAGGCCGG
190 200 210 220 230 240

1450 1460 1470 1480
 TAAATAGCAATTAGTCTACGACCTACGAGATCTCTCTCCCTCCCTCGAATTTAATTTCTTCA
 CAA--GAG--GAGGCT--TCTCCA--AG-----TCTCCAGCTCCGAGGA--GACCTCTTTC-
 250 260 270 280 290

1490 1500 1510 1520 1530 1540 1550
 ACTTGCAATTTGCAGAGATATACACATTTCACTGTGATGATATATGTCTGCAGAGAAAAAGTCTCT
 GCCT--AGCTTATAGCGT---CTGTT--CTG--GAACCATAT---CTTCA-----CTTGGGCTCT
 300 310 320 330 340

560 1570 1580 1590 1600 1610 1620 1630
TTGTTTAAATTACTGGTTTGGATTCACATCTGTTTCCCATTTG-GAATGATTAATACCACTC
CCG-TGAGCTT-GAGGTTCTTG--GCCAGGTGGACCGTT--CAGGCGATCAGTACTT--CTGATGGC
350 360 370 380 390 400

TGAAGTCTGAGAAAACATCTAGAGAGCTAGTATCAGCATCTGACAGGTGAATTG
 1640 1650 1660 1670 1680
 |||||
 TGAAGTCT
 410 X

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4. US-09-700-700-1 (1-1936)
   US-09-105-470B-3 Sequence 3, Application US/09105470E

Initial Score = 42 Optimized Score = 308 Sift Score = 308
Residue Identity = 47% Matches = 415 Mismatches = 465
Gaps = 186 Conservative Substitutions = 0

```

186 Conservative Substitutions

560 570 580 590 600 610 620
TAAACTGGCACTTCTTATTCTTCCTTAAAAATACATGCAATTAAATCCGAATCTATTAAAGAC
||| ||| ||| ||| ||| |||
ATGC----TCAGGATCCGAGAC
X 10

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700 710 720 730 740 750 760
ACA-ATCCTTAGAATCTTTG-CATGCAGAGAGGTAAAGAGTATTGGATTTCACAGAGGAAGAAC--ACA
TCACCTCTTCTCATCAGAGACATCTTCGCG---GACGGCGCGACAGCGCAAGCGCGCGCAGCAGCAGCA

770 780 790 800 810 820 830
GCGCAGATTA-AGGCGCAGGCTTACTAGGCTG-TCCAGT-GAGGGCTCATGGTGGCAGATCGAATAA
GC-CAGA--GACAGTCCGA-----CCCGAGCGCGGACGCAAGCAGC-CA--GAGGA--GG-----
150 160 170 180

840 850 860 870 880 890 900
AGGAGAGCTAGGCGCCCTGGGGAACCC--GTCCA-CTTAGCAAGCAAGGAGCTGAGTGAACCTTTTGGAGGAA
ACGAGGCC--GGCGCGGAGGCCCAAGCAAGCAAGCTAGTGA--CCGGGGCC--CCGGGGCC--GGGCTTCTTGG

[illegible]

260	270	280	290	300	310
980	990	1000	1010	1020	1030
TTATTGCTTAATAAGTTC--CCAAATGGTAACTTACCTTACAGAGACATGAGAGAGGCAAGAG					

320 330 340 350 360 370
 AAAAAAAAAAAGGCGCCCTTCAAA-----TTAACAG-CGGCAGAAGCG
 1050 1060 1070 1080 1090 1100 1110
 AAATCGGTGCCTTCATTATTAATCTCTTATCTCAGGTAGTGCTGTAGAGGGAGCATTTAGAAAAA
 |||||

1120 1130 1140 1150 1160 1170 1180
 TGAACACAAGAACATATTCAATGAGAGGTGGCGGTGGAGCTTGGAGCTTTCTTGA CTTCACACCTCCTTA AATCCCTC
 CTCGCCAGACTG-CTCTTC--TCCCA--CA-----CTCAGATGATGAGCT----TGAGA--GGA---AG
 380 390 400 410 420

TTTCAGC--CATCAGAGATAC--CTCTCGGCCCCCTGA--ACGGG--CCACCTGGC--CAATAACTTA---AG
430 440 450 460 470 480

1270 1280 1290 1300 1310 1320 1330
 CTCACGAG-ACC-CAGCT-CTGAGCAGGATATGTCGCAAAATGCGACAT
 490 500 510 520 530
 -GAAG-ATA-TGGTCCAGAAACAGCGCTAT

AAG-11AAWAAAAGTGGCCATTTCACCCCATTTTGTGGTTTGCGTCCACATTCGATGTTGCAATGC
 AAGCTAAGCCGAAH---GGAGCTCTC-CTGGAGCTGGGAGATTGG-----AGA-AGCAGCTCCCTCTTTTGC
 540 550 560 570 580 590

CACCTGCTGCTGACACCGACCGAGTAC-
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[illegible]

1470 1480 1490 1500

[illegible]

CCCATACNTG-TAANGCNTGG-6GC---ANNGGAGGCCGAGTTTGTGTAANGGCAGCTCCA-----
390 400 410 420 430 440

1300 1310 1320 1330 1340 1350 1360
 TTTCTGTGTTGGGCTCCACATGGAATGTCACGCTGCTGACACCGGACTACTAG--C
 -----GG--TGAACAC--CAT--AAGATCA--AANG--GC--CTTNC--CCAGGGTGTTCATGAA
 450 460 470 480 490 500
 1370 1380 1390 X 1400 1410 1420 1430
 CAGCACAAGAGGAGGT--AGCCTGAATGCTTCTGCTTTACATTTCTTTAAATAGCATTTAGTGC
 AAGCACAAGGGGCAAGCTCAGACCAAAAGN
 510 520 530 X
 1440
 TCAGTCCCT

7. US-09-700-700-1 (1-1936)
 US-09-105-470B-3 Sequence 30, Application US/09105470B

Initial Score = 33 Optimized Score = 152 Significance = 0.64
 Residue Identity = 52% Matches = 191 Mismatches = 115
 Gaps = 61 Conservative Substitutions = 0

AGAAATGAAGGGCCAGGCTTACTAGAGCTGTCCAGTGGAGGGCTCATGTGGGACATGAAAGAGCGAGC
 780 790 800 810 820 X 830 840
 X GGAAGCTG--AGCCAG--AGC
 X 10
 850 860 870 880 890 900 910
 CTAGGCGCTTGGGAGCCAGTCCACTGAG--CA--AGCA--AGGAGTGAAGCTTTGGAGAAAGAGCT
 C--AGACC--AGATCTCAGAACTTGGGTCTATGCTATGAGAGCTGCCGA--CACTCTGAG--AG--CT
 20 30 40 50 60 70 80

920 930 940 950 960 970
 AAGAAAAGG---AAACCATCTTAACACAAAGAACTGCTCAATGCTTTGGAACTGTGTTAT
 CAGCGGCTGGGTCAAC--TTCTGCGACAC---TGCCACTGT--CGTTACTTTGG---CT--TTCTAGA
 90 100 110 120 130 140

980 990 1000 1010 1020 1030 1040
 GCTTAATATGGGCCCA--AAATGGATACCTAGACTTCAGAGAGATGAGAGAGAGCAAGAAATC
 GCC--AATATCTTGGCCATGAATGGTACTGCTTACTTCCAGGTAT--TTTGAGAAAGAG--TGAGATG
 150 160 170 180 190 200

1050 1060 1070 1080 1090 1100 1110
 TGGCTGTCTTCAT--TTTCATCTGTATCTCAGGTAGCTGTAGAGGGGA--GACATTAGAAAAATGA
 AAGTCAACAGTATATATATCTGTCGTGCC---TGCCCTGT--GTGGGAGTGAAC--AGATGATTTTG
 210 220 230 240 250 260 270

1120 1130 1140 1150 1160 1170 1180 1190
 AACACAAAACAATTAATAGAGTACGCTGAGGAGCTCTCTTCACTCCACTACTTATTCGGTT
 GACA--GACCCAGAGCT-----CGCTG--GGCATCTG--GTCTT--TCTTCA
 280 290 300 310 X

AGTGAAGAAACCTTCAATTTCTTTATTGAAGG

8. US-09-700-700-1 (1-1936)
 US-09-105-470B-2 Sequence 26, Application US/09105470B

Initial Score = 28 Optimized Score = 54 Significance = 0.32
 Residue Identity = 50% Matches = 62 Mismatches = 50
 Gaps = 10 Conservative Substitutions = 0

1070 1080 1090 1100 1110 1120 1130 1140
 TTTCTGTATCTCAGTGAAGCTGTAGAGGGAGACATTAGAAAAAATGAACAACAACAATTAATTAATG

1150 1160 1170 1180 1190 1200 1210
 AGATAGCGAGGCGCTGGAGTCTCTTGACTTCACTTAATTCGTTAGTGAACCTTTCAATTTTC
 AATATGTTGA--CTTGTAG--CGATTA--CAATTAAGATGATCCCAATTTGTAG--CGATTAACA--TTTC
 20 30 40 50 60 70 80

1220 1230 1240 1250 1260 1270 1280
 TTTTATTAGAGGCGCAGCTTACTGTGTGTGCAAAATTTCCAAACATTAATTAAGAAAGTTGGCAATTT
 ACACATTAAGAGAGAAATTAATATATG
 90 100 110 X

1290
 CACCCC

9. US-09-700-700-1 (1-1936)
 US-09-105-470B-2 Sequence 28, Application US/09105470B

Initial Score = 25 Optimized Score = 219 Significance = 0.13
 Residue Identity = 46% Matches = 276 Mismatches = 221
 Gaps = 96 Conservative Substitutions = 0

410 420 430 440 450 460 470 480
 CCTAATTAGCGCTGCTTATTATTAGCCGAGATCTGTCTTTTNTGNTTTTNTTTTCCGTCTCC
 TTTTATTTCCCGTCCGACCTCC
 X 10 20

490 500 510 520 530 540 550
 AAAGCTTATCTGTCTTGACTTTTAAAGTTGGGCGAGATTCTTAATTTGGCTTAAAGACATGATT
 GGAG--TTTAT--TC--ACTT--CCAGCGTACTGGGCTG--GACCA--GCTTGTGGCAT--CCGA
 30 40 50 60 70

560 570 580 590 600 610 620
 TTTAAACTAGGCACTTCTTATTTCTTCTTTAAATATACATAGCATTAATCCAAATCTTATTAAAG
 TTCAGCTCCA--GCAGATCCAGGTCCT-----ATCC--AGCATGGGCGGCGACCGCTGTCAAG
 80 90 100 110 120 130

630 640 650 660 670 680 690
 ACTGACAGCTTGA--GAAGT--CACTACTGCATTTATAGACCTTCTGT--GTTTGTCTTTACGTTT
 CTCTGGC--CTTCAGGAATCTTCGAGCTGTCCTTCTCCTGAAAGTGGGCTGCGGCTCTG--GGTCCGTT
 140 150 160 170 180 190 200

700 710 720 730 740 750 760
 GAACTGACAAATCTTGAATCTT--TGCATGCA--AGAGATGAAGGATTTGATTTTTCACAGAGAG
 -CTGGCT--CCAGTTCGCGCTGTGTCTGC--TTCAAGCCTCGGATTCACACTCTGTGCTGCTCG--GCTCC
 210 220 230 240 250 260 270

770 780 790 800 810 820 830
 AACACAGCGCAGATGAAGGCGCAGGCTTACTGAGGCTGTCAATGAGAGGCTCATGGTGGACATGAA
 GATTACG--CTCTTTAGAGGCTCAGCTTCCAG--CTGTG--GCTCTCG--GGTCCCG--GGTCCCG--
 280 290 300 310 320 330

840 850 860 870 880 890 900
 AGAAGGAGCTTGAAGCTCTGGGAGGCCA--GTCCATGTGCAAGCAAGGAGTGAAGTCTTTTGCAGGA
 -GATTGACCC--GCTTCGAGCGCTCAGGCCCTCCGCTACGTCAGGAGTCTGA--AGC--TCG--GG--
 340 350 360 370 380 390

910 920 930 940 950 960 970
 AAAGGCTTAAGAAAGAAACCATTTCTTAAACACAAACAAGAACTGTCCAAATGCTTTGGGAATGTTT
 CAACCGGGCATGTGTGTCACCGAGCGGGTGC--CTCC-----GGGTCAAGTGTGGCTGGGATGAGGGTCTC

980 990 1000 1010 1020 1030 1040 X
 ATTCCTATTAAAG-GGTCCCCAAATGGGTAACTTGAAGAGAAATGGCGAGAGCGAAGGAGAAAA
 |||||
 ATAGC-----TGGCGTCC-----GGTAGCCCGGC-CCAGTCTCGCGAGTGGAAAGC--GGG
 460 470 480 490 500
 1050 1060 1070 1080 1090
 TCTGGCTGCTCTTCCATTTCATTCTGTATTCTCAGGTGAAGCTGG

10. US-09-700-700-1 (1-1936)
US-09-105-470B-1 Sequence 16, Application US/09105470B

Initial Score	=	12	Optimized Score	=	14	Significance	=	-0.71
Residue Identity	=	53%	Matches	=	14	Mismatches	=	12
Gaps	=	0	Conservative Substitutions	=	0			

180 190 200 210 220 230 240
 GCTAGGGGCTTTCATTTTATTATGTAGAAAGTGAAAGCCCTTCTCAACTTTTTCCCTTGGCGTAG
 | |||||
 GCAGCTTTTACCCAAAAGCTTG
 X 10 20

X 250 260 270 280 290
 GAGAAATTGAAATCAGAA GTTCTCGAGTTTCAGGCTATCATATATAC TGTAT
 |
 GGCT
 X

11. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence

-470B-2 Sequence 20, Application US/09105470E

Initial Score	=	11	Optimized Score	=	15	Significance	=	-0.77
Residue Identity	=	61%	Matches	=	16	Mismatches	=	8
Gaps	=	2	Conservative Substitutions	=			=	0

820
ATGGGTGGGACATGGAAAAGAGGACCTAGGCGCTGGGGAGCCAGTGCACATGCAAGCAAGGAGCATCA
840
860
880
900
CACTGCCAGTCATAGTG--TTC
X 10 20

890 900 910 920 930 940
GTGAGCCTTTTGACGAAAGCTAAGAAAAAGCAACCATCTTAATAACACAA
|||
TTGA
X

12. US-09-700-700-1 (1-1936)

[illegible]

Initial Score	=	11	Optimized Score	=	13	Significance	=	-0.77
Residue Identity	=	48%	Matches	=	13	Mismatches	=	14
Gaps	=	0	Conservative Substitutions	=	0			

1530 1540 1550 1560 1570 1580 1590 1600
TTGTGTGCAGNAAAAAGTGTCTTTGTTAAATTACTTGTAATCAATCCCTTTTCTT
GCGGATTCATGCTCAGGATTC
X 10 20

1610 1620 1630 1640 1650
 CCCATTGGAAGTACTGATTCATTAAACCATCTCTGAACACTGCTAGAGAAACATCTGAGAG
 CCGAG
 X

13. US-09-700-700-1 (1-1936)

US-09-105-470B-2 Sequence 24, Application US/09105470B

```
Initial Score = 10 Optimized Score = 13 Significance = -0.84
Residue Identity = 70% Matches = 14 Mismatches = 5
Gaps = 1 Conservative Substitutions = 0
```

[illegible]

240 250 260 270 280
GGGCTGAGAAATTAGAATCAGAAGTTTCCTGGAGTTTCAGGCTATC

14. US-09-700-700-1 (1-1936)
US-09-105-470B-2 Sequence 22, Application US/09105470B

Initial Score	=	9	Optimized Score	=	9	Significance	=	-0.90
Residue Identity	=	60%	Matches	=	9	Mismatches	=	6
Gaps	=	0	Conservative Substitutions	=			=	0

TTTCTGTGTTTGAGCTCCACATGCAATGATGTTCAATGCCAGTGTCTGCTGAACCCGACCGGAGTACTAGCA	1300	1310	1320	1330	1340	1350	1360
						X	
ACACTAATTGGAGGC							
X						10	X

1370	1380	1390	1400
GCACAAAGGCAGG	GTAGCTGAAT	TGCTTCTG	CTCTTACA

15. US-09-700-700-1 (1-1936)

US-09-105-470B-1 Sequence 19, Application US/09105470B

Initial Score	=	9	Optimized Score	=	15	Significance	=	-0.90
Residue Identity	=	56%	Matches	=	17	Mismatches	=	9
Gaps	=	4	Conservative Substitutions	=	0			

70 80 90 100 110 120 130 140
AGACAGCTGTATTAACAGAACTCACTGCAGAGGAGGCGCGGCCACGAGGAACTCCGCTGTCCAGACT
GCAGATC---CTTACCCAAA
X

150 160 170 180 190
CAGGGGCGCTAAGAGAGGCTCTCCACACTGCTCTAGGGGCTGTTGCATTTTTTATTAG
|||||
GCTGGGCT
20 X

16. US-09-700-700-1 (1-1936)
US-09-105-470B-1 Sequence

US-09-105-470B-1 Sequence 18, Application US/09105470B

Initial Score	=	9	Optimized Score	=	15	Significance	=	-0.90
Residue Identity	=	56%	Matches	=	17	Mismatches	=	9
Gaps	=	4	Conservative Substitutions	=	0			

70 80 90 100 110 120 130 140
AGACAACTGTATAAACAGAACTCACTGCAGAGGGGCGGGCCAGGGAATCTCCGCTGTGCCAACA
|||||
GCGATC-----CTTACCCAAAA
X 10

150
160
170
180
190
CAGGGCCCTAAGAGGGTCCACACTGCTGCTAAGGGCTGTTCATTTTATTAAG
|||
GCTGGGCT
X
20

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file 020956_X_4399313.res made by spaula on Fri 12 Sep 103 15:35:26-PDT.

Query sequence being compared:	US-09-020-956-53	(1-484)
Number of sequences searched:		1
Number of scores above cutoff:		1

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2050      2060      2070      2080      2090      2100      2110
350      360      370      380      390      400
TG-TTGGCTCTCCCTATGAT-TGGAGGT---CNGTA-----AATNCAAAACATATCCACTC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TCCTTCATTTTCAATCTGTATCTCAGGTGAGCTGTAGAGGGGAGACATTAAGAAAAAATGAACACAA
2120      2130      2140      2150      2160      2170      2180
410      420      430      440      450      460
AACACTT-CT--T---TTCNCGTA--NCT-TGANTCTGTATTCAGGA--NCAGCGGATGGAATGGGC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AACAATTACTAATGAGGTAGCGCTGGAGCTGGAGTCTCTTGACTCCACTTAATTCCG-TTAgTGAG-
2190      2200      2210      2220      2230      2240      2250
470      480      X
CAGCCNCGGATGTCCANT
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AAACCTTTTCAATTTCTTTTATTAGAAAGGCCACCTTACTGTGTGGCAAAATGCCAAACATTAAGTTAA
2260      2270      2280      2290      2300      2310      2320
```